

Letter No.: 12557-003001  
 Applicant(s): Andrew P. Kloek et al.  
 MATODE PGM-LIKE SEQUENCES

1 gtt taa tta ccc aag ttt gag ATG GAC AAA TAT GTT CAA CAA AAA GTC TGT CTT  
 M D K Y Q N V Q Q K V C L

61 GTA GTT ATT GAT GGA TGG GGC CTT TCC GAT GAA CAA CAC GGG AAT GCA ATT GCT AAA GCT  
 V V I D G W G L S D E Q H G N A I A K A

121 AAA ACG CCT ATT ATG GAC AAA CTT TGT TCT GGA AAT TGG CAA AAA TTG GAA GCA CAC GGT  
 K T P I M D K L C S G N W Q K L E A H G

181 CTT CAT GTT GGA TTG CCA GAA GGC TTA ATG GGA AAT TCT GAA GTT GGA CAT TTG AAT ATA  
 L H V G L P E G L M G N S E V G H L N I

241 GGA GCT GGA AGA GTT ATT TAT CAA GAT ATT GTT CGA ATT AAT TTG GCT GTT CAA CGA AAC  
 G A G R V I Y Q D I V R I N L A V Q R N

301 GAG TTT GTT ACA AAT CCT CAG ATT GTT GCA TCA GCT GAG CGT GCA AAG AAG GGG AGT GGT  
 E F V T N P Q I V A S A E R A K K G S G

361 CGA TTG CAT TTA TTA GGA CTG GTT AGC GAT GGT GGT GTC CAC TCT CAT ATT GAT CAT CTT  
 R L H L L G L V S D G G V H S H I D H L

421 TTT GCG TTG ATA CGT GCA TTT AAA CAA TTA CAA GTG CCA AAG GTT TTC ATT CAC TTT TTT  
 F A L I R A F K Q L Q V P K V F I H F F

481 GCT GAT GGT CGA GAT ACT TCG CCA ACA AGT GGA GCT GGT TAT CTT GAA CAA CTT CTT CAA  
 A D G R D T S P T S G A G Y L E Q L L Q

541 TTT ATT GCT TCG GAA AAG TAC GGA GAA TTG GCT ACT ATT ACT GGA CGT TAT TAT GCA ATG  
 F I A S E K Y G E L A T I T G R Y Y A M

601 GAT AGG GAC AAA AGA TGG GAG CGT ATT AAG ATG GCT TAT GAG GCA ATT GTT GGA GGT ATT  
 D R D K R W E R I K M A Y E A I V G G I

661 GGA CAA AAA GCC ACC GTT GAT AAG GCT GTC GAT GTT AGA GAG CGA TAT GCT CAA TCT  
 G Q K A T V D K A V D V V R E R Y A Q S

721 GAG ACT GAC GAA TTT CTG AAA CCA ATT GTT TTT TCG GAC GAT GGG CGA GTA AAA GAT GAC  
 E T D E F L K P I V F S D D G R V K D D

781 GAT ACT CTT ATT TTC TTC AAT TAT CGT GCT GAT CGT ATG CGT CAA ATT TGT GAA TGT TTG  
 D T L I F F N Y R A D R M R Q I C E C L

841 GGT CTC GAA CGT TAT AAA GAT CTT AAT AGT TCG GTT CCT CAC CCT AAA AAT ATT CAG ATT  
 G L E R Y K D L N S S V P H P K N I Q I

FIGURE 1A

901

AGT GGG ATG ACC CAA TAC AAT AAA GAG TTT CCA TTT CCA TCG TTA TTC CCA CCT GTG ACT  
S G M T Q Y N K E F P F P S L F P P V T

961

CAT ACT AAT GTG CTT GCT GAA TGG CTT GCT TCT CAA GGA GTT ACT CAA TTT CAC TGT GCG  
H T N V L A E W L A S Q G V T Q F H C A

1021

GAA ACT GAG AAG TAT CCT CAT GTT ACC TTC TTC TTT AAT GGT GGT CGA GAA GTT CAA TTC  
E T E K Y P H V T F F F N G G R E V Q F

1081

CAA GAT GAA GAG CGT TGT ATG GTT CCG TCA CCA AAA GAA GTT GCT ACA TAT GAT TTA AAA  
Q D E E R C M V P S P K E V A T Y D L K

1141

CCA GAA ATG AAT GCT GCT GGA GTT GCC GAA AAA ATG GTC GAG CAA ATT GAG TCA GGC AGG  
P E M N A A G V A E K M V E Q I E S G R

1201

CAT CCT TTG GTT ATG TGC AAT TTT GCG CCT CCT GAC ATG GTT GGA CAT ACT GGT AAA TTT  
H P L V M C N F A P P D M V G H T G K F

1261

GAA CCT GCC GTC AAA GCA TGT CAA GCT ACT GAC GAG GCA ATT GGA AAG ATA TTT GAA GCA  
E P A V K A C Q A T D E A I G K I F E A

1321

TGC CAA ACT TAT AAT TAC GTT CTT ATG GTT ACT TCC GAT CAT GGA AAT GCT GAG AAG ATG  
C Q T Y N Y V L M V T S D H G N A E K M

1381

ATT GCT CCC GAT GGT AGT GAA CAT ACT GCA CAT ACC TGC AAT TTG GTC CCA TTT ACT TGC  
I A P D G S E H T A H T C N L V P F T C

1441

TCT TCC AAA ACA TTT GTT TTT AAA TCG ACT CCA CCT ACT GGA GAT GAT GGC AAA GAA CGT  
S S K T F V F K S T P P T G D D G K E R

1501

GCA CGA GCC TTA CGT GAT GTT GCA CCG ACT GTT CTA CAA TTA ATG GGC TTA CCT GTA CCG  
A R A L R D V A P T V L Q L M G L P V P

1561

CCG GAG ATG GAT GGC GTT CCT TTA CTT GAA CAG AGA GGA TAA gaa gtt aat tga caa tag  
P E M D G V P L L E Q R G \*

1621

gaa ata aat atg agc tgc tat tac aag caa ttt taa aaa ttt tag taa aac gag taa ttt

1681

ttg ata tat aca tat tta gaa atc tcc gtt ata aaa att

FIGURE 1B

1 Met phe val ala leu gly ala gln ile tyr arg gln tyr phe gly arg arg gly met ala  
21 met ala asn asn ser ser val ala asn lys val cys leu ile val ile asp gly trp gly  
41 val ser glu asp pro tyr gly asn ala ile leu asn ala gln thr pro val met asp lys  
61 leu cys ser gly asn trp ala gln ile glu ala his gly leu his val gly leu pro glu  
81 gly leu met gly asn ser glu val gly his leu asn ile gly ala gly arg val ile tyr  
101 gln asp ile val arg ile asn leu ala val lys asn lys phe val thr asn glu ser  
121 leu val asp ala cys asp arg ala lys asn gly arg leu his leu ala gly leu  
141 val ser asp gly gly val his ser his ile asp his met phe ala leu val lys ala ile  
161 lys glu leu gly val pro glu leu tyr leu his phe tyr gly asp gly arg asp thr ser  
181 pro asn ser gly val gly phe leu glu gln thr leu glu phe leu glu lys thr thr gly  
201 tyr gly lys leu ala thr val val gly arg tyr tyr ala met asp arg asp asn arg trp  
221 glu arg ile asn val ala tyr glu ala met ile gly gly val gly glu thr ser asp glu  
241 ala gly val val glu val val arg lys arg tyr ala ala asp glu thr asp glu phe leu  
261 lys pro ile ile leu gln gly glu lys gly arg val gln asn asp asp thr ile ile phe  
281 phe asp tyr arg ala asp arg met arg glu ile ser ala ala met gly met asp arg tyr  
301 lys asp cys asn ser lys leu ala his pro ser asn leu gln val tyr gly met thr gln  
321 tyr lys ala glu phe pro phe lys ser leu phe pro pro ala ser asn lys asn val leu  
341 ala glu trp leu ala glu gln lys val ser gln phe his cys ala glu thr glu lys tyr  
361 ala his val thr phe phe asn gly gly leu glu lys gln phe glu gly glu glu arg  
381 cys leu val pro ser pro lys val ala thr tyr asp leu gln pro glu met ser ala ala  
401 gly val ala asp lys met ile glu gln leu glu ala gly thr his pro phe ile met cys  
421 asn phe ala pro pro asp met val gly his thr gly val tyr glu ala ala val lys ala  
441 cys glu ala thr asp ile ala ile gly arg ile tyr glu ala thr gln lys his gly tyr

FIGURE 2A

461

ser leu met val thr ala asp his gly asn ala glu lys met lys ala pro asp gly gly  
481  
lys his thr ala his thr cys tyr arg val pro leu thr leu ser his pro gly phe lys  
501  
phe val asp pro ala asp arg his pro ala leu cys asp val ala pro thr val leu ala  
521  
ile met gly leu pro gln pro ala glu met thr gly val ser ile val gln lys ile

**FIGURE 2B**

1 *M. incognita* PGM

2 *C. elegans* PGM

1 . . . . . MD KYQN VQOKWCLVAVLDGNGLTSDEQHGNAMAKAKKTPYMDK : 40  
2 MFVALGAQIYRQYFGRRGMAANNSSVANVCLIVLDGNGVSEDPYGNALNAAQKTPYMDK : 60

1 ICGSGNWOKLEAHGLHVGLPEGLMGNSEVGHLNIGRVLWQDIVRNLAVERNE SMTNPQ : 100  
2 ICGSGNWQLEAHGLHVGLPEGLMGNSEVGHLNIGRVLWQDIVRNLAWKNNK SMTNES : 120

1 IVASADRAKKGSGRILHLLGLVSDGGVHSHIDHLFAILRAFKQDQMPKMEPHEADGRDT : 160  
2 IVDACDRAKNGNERIHLAAGLVS DGGVHSHIDHMFIAIVKAIKE LGVDE LYAFHFVGDGRDT : 180

1 PTSGAGYVPLQLLQHASEK. KGE LAMITGRYYAMDROKRWERIKMAMVEAVVGGIGOKATV : 219  
2 PNSGVGEHINOTLEREELKTTGKGKATVVGRYYAMDRONRWERINVAEYAMECCGVGETSDE : 240

1 DKA VDWVRE RYAQSETDDEFLKPPLMFS. DDGRVKDDDTILEENMRADRMRCCECIGIERY : 278  
2 AGVVEVYVRK RYAADETDEFLKPPLQGEKGRVQNDDTILEEDYRADMRELSAAMGMDRY : 300

1 KDLNNSSMPHPKNLQIISGMTOYNKEPPPEPSLFPPLVDTNTVLAEPWLANSOGMTOPHCAELTKH : 338  
2 KDCNSKLAHPNSNLOVYGMTOYKAEPPEKSLSPPPASNKNVLAEPWLAEOKVSOOPHCAELTKY : 360

1 PHVTEEEENGGRPVQFQDEERCMVPSPKEVATYDJKPRMNAGVAEKMVPGQPSGRHPLVM : 398  
2 AHVTEEEENGCLEKOPEGEEROTVPSPK. VATYDJKPRMSAGVAADGMTEQMLAESTBPFAM : 419

1 CNEAPPDMVGHTGKRPAPAVKACQATIDEAEGKIEEACOTYNNVLMVLSDHQNAEKMKIAPDG : 458  
2 CNEAPPDMVGHTGVKEAPAVKAGEATDIAGRIYEATOKHGSKMWVADHICNAEKMKIAPDG : 479

1 SETTAHTGTLVDFTCSSKTPEVKSTPPTGDDGKERAARAIERDVAPPTVQEMGIPVPPBMDG : 518  
2 GKHTAHTGTYRPLTLSPGFKFVDP.....ADRHPATCDVAPTVIAEMGIPQBAEMTG : 532

1 MPLEEQRG : 526  
2 MSQKIZ : 539

FIGURE 3